

Q590
11/20

#2 2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/987,025DATE: 11/19/2001
TIME: 11:09:53Input Set : A:\SeqList.txt
Output Set: N:\CRF3\11192001\I987025.raw**ENTERED**

4 <110> APPLICANT: Boronat, Albert
 5 Campos, Narcisco
 6 Kishore, Ganesh M.
 8 <120> TITLE OF INVENTION: Nucleic Acid Sequences Involved in
 9 Isoprenoid Synthesis
 11 <130> FILE REFERENCE: 17142/02/US
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/987,025
 14 <141> CURRENT FILING DATE: 2001-11-13
 16 <150> PRIOR APPLICATION NUMBER: 09/549,787
 17 <151> PRIOR FILING DATE: 2000-04-14
 19 <150> PRIOR APPLICATION NUMBER: 60/129,899
 20 <151> PRIOR FILING DATE: 1999-04-15
 22 <150> PRIOR APPLICATION NUMBER: 60/146,461
 23 <151> PRIOR FILING DATE: 1999-07-30
 25 <160> NUMBER OF SEQ ID NOS: 13
 27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 3400
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Arabidopsis sp
 34 <400> SEQUENCE: 1

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36	caaatccaga ttcctttctt atcatcatct ctctctctca cactgtttat ctgattcgctc	120
37	ttctctgata atcaagagta gtagtgcggt tctctggaaa atattcgatt tttaaaagac	180
38	tctgatgatg acattaaact cactatctcc agctgaatcc aaagctatct ctttcttgga	240
39	tacctccagg ttcaatccaa tccctaaact ctcagggttc ttcttcttcc tctcttcttt	300
40	cctcctcctt ggtcaactct cttttcgatt aaagttgcaa actttcatta gttgtcttag	360
41	gctcttgatg atttctctat ctaggtaatc tggtatttct tcaattcgat ttttttgggt	420
42	ttgctttagg tcttagaggt ttaaatttta catctttgga gtgtttcaca ggtgggttta	480
43	gtttgaggag gaggaatcaa gggagagggt ttggaaaagg tgtaaagtgt tcagtgaag	540
44	tgcagcagca acaacaacct cctccagcat ggctgggag agctgtccct gaggcgcctc	600
45	gtcaatcttg ggatggacca aaaccatct ctatcggttg atctactggt tctattggca	660
46	ctcagggtttt atttcgatta aggcattatt gtgcagttct tgagtatgac cagactttaa	720
47	gtttgtctta tgaatgacta gactcataga agaagatat tttttctta ctgagttatt	780
48	gttgcatcat ttttatcgac aagaacttcc attttgcaga cattggatat tgtggctgag	840
49	aatcctgaca aattcagagt tgtggctcta gctgctggt cgaatgttac tctacttgct	900
50	gatcaggtaa gttggcttca ttgtaaaaa aattagtatt gagtctctcc aatttgcat	960
51	tcagaccact tggaattcag tttaattctc agttcagtg tagtatcata agcaagatag	1020
52	tattaactcg ttatgtatca gatcaaacca gagaaatcag gttctggttt aggcttttgc	1080
53	ttctgcaatc tcaagaaatc tctatagtat ggttctgtga ttctattttg aatggtggca	1140
54	ggtaaggaga tttaagcctg cattggttgc tgtagaaac gagtcaactga ttaatgagct	1200
55	taaaaggagct ttagctgatt tggactataa actcgagatt attccaggag agcaaggagt	1260
56	gattgagggt agttcatttg ttagttttga ttgtagtgta gataggtttt tacttattat	1320
57	gttcatcaac aggttgcccc acatcctgaa gctgtaaccg ttgttaccgg aatagtaggt	1380
58	tgtgcgggac taaagggtata tactctaatt tttgtttatt aaaccttatt aagaggatat	1440
59	gaaaaaagaa agttgcagat gataaagctt gttgcttatt tttactgcag cctacggtg	1500
60	ctgcaattga agcaggaaag gacattgctc ttgcaaacaa agagacatta atcgagggtg	1560

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61 gtccttttcgt gcttccgctt gccacaacaa ataatgtaaa gattcttccg gcagattcag 1620
62 aacattctgc catatttcag gtatcacaaa tcacatagaa ttaagtacct caactttcat 1680
63 attgagttca gcgttgggtct taatgcaagt tcaacctctg gcaatttgag tgaaaaatct 1740
64 tcttttatgt tctctagtgt attcaagggt tgcctgaagg cgctctgcgc aagataatct 1800
65 tgactgcac tgggtggagct tttaggtttg tttcgaatatt cttctctctc tgcatagact 1860
66 ttttttcttc tcaattctcg tttgggttaat ggaaactttt cactggattt tgaaaaaggg 1920
67 attggcctgt cgaaaagcta aaggaagtta aagtagcgga tgcgttgaag catccaaact 1980
68 ggaacatggg aaagaaaatc actgtggact ctgctacgct tttcaacaag gtttaagatta 2040
69 ttttctccta aggttaaaact ctgattttga aaataccttt gatcaaggta gatgagttct 2100
70 tgattttttg aaacagggtc ttgagggtcat tgaagcgcat tatttgtttg gagctgagta 2160
71 tgacgatata gagattgtca ttcatccgca aagtatcata cattccatga ttgaaacaca 2220
72 ggtcttgctg aaacattact aactaaaatta ttatttttcc ggttttaaaa aaataactgt 2280
73 ataacatgta tttgttttgt tccacaggat tcatctgtgc ttgctcaatt ggggtggcct 2340
74 gatatgcgtt taocgattct ctacaccatg tcatggcccg atagagttcc ttgttctgaa 2400
75 gtaacttggc caagacttga cttttgcaag taagctaacc acatttatat actctctgtt 2460
76 tatcaagtgt gaagctaagc ttagttgaaa attttaatta tcaccaagaa aagttcccca 2520
77 atcttgtttt cagtttggtt ttaggttggt tagataagat aaaaaatgaa accgaatcgg 2580
78 tcttcgggtt ggttttgcaa ttggttattt tgctactgtt ttggtgtgga tcagttaaac 2640
79 tgggttagga cactgcctt atctatcagc attcagcacc taaaaccaa agttgtttac 2700
80 aattgtggat tttggcagac tcggttcatt gactttcaag aaaccagaca atgtgaaata 2760
81 cccatccatg gatcttgctt atgctgctgg acgagctgga ggcacaatga ctggagttct 2820
82 cagcgccgcc aatgagaaaag ctgttgaaat gttcattgat gaaaagtaag aattattttt 2880
83 cagttttgag catctcaatg aagttcttga tacgaatcac aattgtttat attctcactt 2940
84 ttgtttacag gataagctat ttggatatct tcaagggtgt ggaattaaca tgcgataaac 3000
85 atcgaaacga gttggttaaca tcaccgtctc ttgaagagat tgttcactat gacttgtggg 3060
86 cagtggaata tgcgcgcaat gtgcagcttt cttctggtgc taggccagtt catgcatgaa 3120
87 gaattggttg ttggaagaac ataaggaagc ttctgaggaa atgttgaaag aagattagt 3180
88 tagagaatgg ggtactactt aatagcgttt ttggcaagga ttatggattg tgtagcta 3240
89 ttatctgtga tccgaacaag ccaaactgat aatttgaaac catttttacc aataaaaccg 3300
90 agcttaattg tttcacatta tatgattaat tacattcatc taagggttct tgaaaagcct 3360
91 ctgagcttca tgagtagagt tcgcatctcc tgttgtcgtc 3400

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93 <210> SEQ ID NO: 2

94 <211> LENGTH: 477

95 <212> TYPE: PRT

96 <213> ORGANISM: Arabidopsis sp

98 <400> SEQUENCE: 2

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99 Met Met Thr Leu Asn Ser Leu Ser Pro Ala Glu Ser Lys Ala Ile Ser
100 1 5 10 15
101 Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
102 20 25 30
103 Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
104 35 40 45
105 Lys Cys Ser Val Lys Val Gln Gln Gln Gln Pro Pro Pro Ala Trp
106 50 55 60
107 Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
108 65 70 75 80
109 Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
110 85 90 95
111 Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu

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112          100          105          110
113 Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
114          115          120          125
115 Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
116          130          135          140
117 Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
118 145          150          155          160
119 Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
120          165          170          175
121 Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
122          180          185          190
123 Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
124          195          200          205
125 Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
126          210          215          220
127 Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
128 225          230          235          240
129 Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
130          245          250          255
131 Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
132          260          265          270
133 Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
134          275          280          285
135 Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
136          290          295          300
137 His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
138 305          310          315          320
139 Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
140          325          330          335
141 Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
142          340          345          350
143 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
144          355          360          365
145 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
146          370          375          380
147 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
148 385          390          395          400
149 Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
150          405          410          415
151 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
152          420          425          430
153 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
154          435          440          445
155 Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
156          450          455          460
157 Asn Val Gln Leu Ser Ser Gly Ala Arg Pro Val His Ala
158 465          470          475
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 25

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162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: Synthetic Oligonucleotide
168 <400> SEQUENCE: 3
169 ctctggatgt catatgaagc aactc 25
171 <210> SEQ ID NO: 4
172 <211> LENGTH: 19
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial Sequence
176 <220> FEATURE:
177 <223> OTHER INFORMATION: Synthetic Oligonucleotide
179 <400> SEQUENCE: 4
180 ccgcataaca ccgccaacc 19
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Synthetic Oligonucleotide
190 <400> SEQUENCE: 5
191 gcacacttcc actgtgtgtg 20
193 <210> SEQ ID NO: 6
194 <211> LENGTH: 20
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Synthetic Oligonucleotide
201 <400> SEQUENCE: 6
202 attcgaacca gcagctagag 20
204 <210> SEQ ID NO: 7
205 <211> LENGTH: 21
206 <212> TYPE: DNA
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <223> OTHER INFORMATION: Synthetic Oligonucleotide
212 <400> SEQUENCE: 7
213 ccagtagatc caacgataga g 21
215 <210> SEQ ID NO: 8
216 <211> LENGTH: 20
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Synthetic Oligonucleotide
223 <400> SEQUENCE: 8
224 ggccatgctg gaggaggttg 20
226 <210> SEQ ID NO: 9
227 <211> LENGTH: 25
228 <212> TYPE: DNA

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229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Synthetic Oligonucleotide
234 <400> SEQUENCE: 9
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237 <210> SEQ ID NO: 10
238 <211> LENGTH: 24
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Synthetic Oligonucleotide
245 <400> SEQUENCE: 10
246 cagtttggct tggtcggatc acag                                24
248 <210> SEQ ID NO: 11
249 <211> LENGTH: 32
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Synthetic Oligonucleotide
256 <400> SEQUENCE: 11
257 ctgagagtgc accatctgcg gtgtgaaata cc                        32
259 <210> SEQ ID NO: 12
260 <211> LENGTH: 34
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Synthetic Oligonucleotide
267 <400> SEQUENCE: 12
268 ggcataatggt gaaacccatc tctatcggtg gatc                    34
270 <210> SEQ ID NO: 13
271 <211> LENGTH: 33
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Synthetic Oligonucleotide
278 <400> SEQUENCE: 13
279 acgaattcat tatgcatgaa ctggcctagc acc                        33

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VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number